

## SEQUENCE LISTING

<110> BUTZKE, DANIEL  
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 MEYER, THOMAS

<120> L-AMINO ACID OXIDASE WITH CYTOTOXIC ACTIVITY FROM  
 APLYSIA PUNCTATA

<130> WEICKM-0046

<140> 10/542,769

<141> 2005-07-20

<150> PCT/EP04/00423

<151> 2004-01-20

<150> EP 03001232.2

<151> 2003-01-20

<150> EP 03026613.4

<151> 2003-11-19

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<170> PatentIn Ver. 3.3

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Tyr	Leu	Arg	Gly	Gln	Ser	Leu	Thr	Lys	Lys	Gln	Val	Lys	Ser	Gly	Asp	130	135	140	
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Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn	
245 250 255	
gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc aac	816
Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn	
260 265 270	
ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat gga caa	864
Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln	
275 280 285	
acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag aga	912
Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg	
290 295 300	

gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat	960
Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn	
305 310 315 320	
cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc ccg	1008
Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro	
325 330 335	
att cct gca agt aaa gtg ttc atg acc ttt gat cag ccc tgg tgg ttg	1056
Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu	
340 345 350	
gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc agc	1104
Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser	
355 360 365	
caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc ctg	1152
Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu	
370 375 380	
atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag ctg	1200
Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu	
385 390 395 400	
aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac cag	1248
Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln	
405 410 415	
gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag gct	1296
Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala	
420 425 430	
tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtg acc gcc gct tcc	1344
Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser	
435 440 445	
cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg	1392
Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg	
450 455 460	
gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca	1440
Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser	
465 470 475 480	
ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga ctt	1488
Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu	
485 490 495	
atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc	1536
Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile	
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Asn Asp Tyr Phe Leu	
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&lt;211&gt; 517

&lt;212&gt; PRT

&lt;213&gt; Aplysia punctata

&lt;400&gt; 6

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Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
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Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
      35           40           45

Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
      50           55           60

Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
      65           70           75           80

Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
      85           90           95

Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
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Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val
      115          120          125

Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val
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Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro
      145          150          155          160

Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe
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Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
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Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
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Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
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Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
      225          230          235          240

Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
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Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
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Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln  
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 Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn  
 305 310 315 320  
 Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro  
 325 330 335  
 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu  
 340 345 350  
 Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser  
 355 360 365  
 Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu  
 370 375 380  
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 385 390 395 400  
 Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln  
 405 410 415  
 Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala  
 420 425 430  
 Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser  
 435 440 445  
 Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg  
 450 455 460  
 Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser  
 465 470 475 480  
 Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu  
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gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct	96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser	
20 25 30	
gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc	144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe	
35 40 45	
acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa	192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu	
50 55 60	
gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct	240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser	
65 70 75 80	
cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga	288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly	
85 90 95	
ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att	336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile	
100 105 110	
gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg	384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg	
115 120 125	
ggc ctt ttt atc att gat gat aag ggt att ctt cgg cag atc act gta	432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val	
130 135 140	
aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt	480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val	
145 150 155 160	
cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc	528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	
165 170 175	
tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa	576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys	
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             20                    25                    30  
 Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe  
             35                    40                    45  
 Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu  
             50                    55                    60  
 Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser  
             65                    70                    75                    80  
 His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly  
                     85                    90                    95  
 Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile  
                     100                    105                    110  
 Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg  
             115                    120                    125  
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val  
             130                    135                    140  
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val  
             145                    150                    155                    160  
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly  
                     165                    170                    175  
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys  
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<400> 21

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<210> 22

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<400> 28  
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<400> 30  
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65					70					75					80



Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val  
                                     85                                    90                                    95

Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro  
                                     100                                    105                                    110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr  
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Gly Tyr Gly Ser Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr  
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           20                  25                  30

Arg	Glu	Phe	Gln	Ala	His	Pro	Pro	Val	Gln	Gln	Xaa	Gln	Glu	Val	Gln
		35					40					45			
Glu	Xaa	Pro	Val	Phe	Arg	Val	Trp	Arg	Xaa	Xaa	Gly	Xaa	Ile	Arg	Cys
	50					55					60				
Gln	Trp	Leu	Phe	Trp	Arg	Val	Pro	Gly	Xaa	Leu	Arg	Arg	Thr	Asn	Gly
65					70					75					80
Ala	Arg	Tyr	Asn	Xaa	His	Arg	Ser	Pro	Glu	Ala	Arg	Ala	Lys	Lys	Thr
				85					90					95	
Gln	Glu	Glu	Lys	Phe	Pro	Asn	Gln	Ile	Xaa	Xaa	Thr	Leu	Met	Gly	Xaa
			100					105					110		
Xaa	Asp	Asp	Gln	Cys	Val	Cys	Glu	Arg	Ile	Met	Leu	Trp	Phe	Met	Met
	115						120					125			
Ser	Cys	Ser	Xaa	Xaa	Tyr	Arg	Leu	Xaa	Arg	Leu	Thr	Arg	Tyr	Arg	His
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<220>  
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 <223> variable amino acid

<220>  
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<220>  
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 <222> (127)  
 <223> variable amino acid

<220>  
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 <222> (138)  
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<400> 44  
 Thr Ala Pro Ala Thr Thr Xaa Ala Pro Ala Glu Pro Thr Cys Glu Lys  
   1                  5                  10                  15  
 Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile  
                   20                  25                  30  
 Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys  
           35                  40                  45  
 Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val  
   50                  55                  60  
 Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala  
   65                  70                  75                  80  
 Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro  
                   85                  90                  95

Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn  
                   100                                  105                                  110  
 Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys  
                   115                                  120                                  125  
 His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys  
                   130                                  135                                  140  
 Thr His Cys Ser Lys Lys Lys Lys Lys  
                   145                                  150

<210> 45  
 <211> 153  
 <212> PRT  
 <213> *Aplysia punctata*

<220>  
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 <223> variable amino acid

<220>  
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<220>  
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<220>  
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<220>  
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<220>  
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<220>  
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<220>  
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<220>  
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 <223> variable amino acid

<220>  
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 <222> (133)  
 <223> variable amino acid

<400> 45  
 Pro Pro Pro Pro Xaa Xaa His Gln Gln Asn Gln Pro Ala Arg Ser  
   1                  5                  10                  15  
 Cys Pro Xaa Gly Ser Thr Trp Xaa Arg Asn Ser Lys Val Pro Glu Ser  
                   20                  25                  30  
 Xaa Val Ser Ser Ser Ser Ala Cys Ser Thr Gly Xaa Arg Ser Ala Arg  
           35                  40                  45  
 Lys Xaa Ser Ile Pro Cys Leu Ala Met Met Arg Xaa His Ser Leu Ser  
   50                  55                  60  
 Val Val Val Leu Ala Cys Ser Arg Xaa Ala Thr Lys Asn Lys Arg Arg  
   65                  70                  75                  80  
 Pro Leu Gln Xaa Pro Gln Lys Pro Arg Ser Gln Ser Gln Glu Asp Pro  
                   85                  90                  95  
 Arg Gly Lys Ile Ser Gln Ser Asn Xaa Val Asn Thr Asp Gly Leu Xaa  
           100                  105                  110  
 Xaa Arg Pro Val Arg Leu Arg Lys Asn His Val Met Val His Asp Val  
           115                  120                  125  
 Met Leu Leu Ile Xaa Val Val Thr Phe Asn Ala Ile Gln Thr Leu Lys  
   130                  135                  140  
 Leu Ile Val Gln Lys Lys Lys Lys Lys  
   145                  150

<210> 46  
 <211> 9  
 <212> PRT  
 <213> Aplysia punctata

<220>  
 <221> MOD\_RES  
 <222> (3)  
 <223> Ile or Val

<400> 46  
 Asp Gly Xaa Cys Arg Asn Arg Arg Gln  
       1                  5

<210> 47  
 <211> 14  
 <212> PRT  
 <213> Aplysia punctata

<400> 47  
 Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg  
       1                  5                  10

<210> 48  
 <211> 7  
 <212> PRT  
 <213> Aplysia punctata

<400> 48  
 Val Phe Glu Tyr Ser Asp Arg  
       1                  5

<210> 49  
 <211> 16  
 <212> PRT  
 <213> Aplysia punctata

<220>  
 <221> MOD\_RES  
 <222> (3)  
 <223> variable amino acid

<400> 49  
 Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile  
       1                  5                  10                  15

<210> 50  
 <211> 10  
 <212> PRT  
 <213> Aplysia punctata

<400> 50  
 Val Ile Scr Glu Leu Gly Leu Thr Pro Lys  
       1                  5                  10



<210> 51  
 <211> 11  
 <212> PRT  
 <213> Aplysia punctata

<220>  
 <221> MOD\_RES  
 <222> (5)  
 <223> variable amino acid

<400> 51  
 Val Ile Leu Ala Xaa Pro Val Tyr Ala Leu Asn  
       1                  5                  10

<210> 52  
 <211> 8  
 <212> PRT  
 <213> Aplysia punctata

<400> 52  
 Val Phe Met Thr Phe Asp Gln Pro  
       1                  5

<210> 53  
 <211> 10  
 <212> PRT  
 <213> Aplysia punctata

<400> 53  
 Ser Asp Ala Leu Phe Phe Gln Met Tyr Asp  
       1                  5                  10

<210> 54  
 <211> 18  
 <212> PRT  
 <213> Aplysia punctata

<400> 54  
 Ser Glu Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly  
       1                  5                  10                  15

Leu Lys

<210> 55  
 <211> 21  
 <212> PRT  
 <213> Aplysia punctata

<400> 55  
 Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gln Tyr Asn Gln Val  
       1                  5                  10                  15

Thr Glu Pro Leu Lys  
20

<210> 56  
<211> 28  
<212> PRT  
<213> Aplysia punctata

<400> 56  
Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn Ser Ala Tyr Met  
1 5 10 15

Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu  
20 25

<210> 57  
<211> 8  
<212> PRT  
<213> Aplysia punctata

<400> 57  
Arg Val Gly Gly Arg Leu Phe Thr  
1 5

<210> 58  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 58  
tcctaacgta ggtctagacc tgttgcatTT tttttttttt ttttt

45

<210> 59  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<220>  
<221> modified\_base  
<222> {17}  
<223> a, c, g, t, unknown or other

<400> 59  
tcgtgttcga rtactengay cg

22

<210> 60  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 60  
 ctgtaggtct agacctgttg ca 22

<210> 61  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 61  
 ccgtgtagat ctactgccca ta 22

<210> 62  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 62  
 ccgttgagtt gtagacct 18

<210> 63  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<220>  
 <221> modified\_base  
 <222> (24)  
 <223> inosine

<220>  
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 <222> (25)  
 <223> inosine

<220>  
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 <223> inosine

<220>  
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 <223> inosine

<220>  
 <221> modified\_base  
 <222> (34)  
 <223> inosine

<220>  
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 <222> (35)  
 <223> inosine

<400> 63  
 ggccacgcgt cgactagtagtac gggnnngggnn gggnnng

36

<210> 64  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 64  
 aattggccac gcgtcgacta gtac

24

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 65  
 aattctcgtc tgctgtgctt ctcct

25

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 66  
 gacttagagg aagtagtcgt tga 23

<210> 67  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 67  
 ctggttatgcc agatggtcag 20

<210> 68  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 68  
 gataccaaaag gaatgttcac g 21

<210> 69  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 69  
 caagaaggag ggtgacctga 20

<210> 70  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 70  
 ttcggtgaag tcctactcta cg 22

<210> 71  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       primer  
  
 <400> 71  
 ggtatcgtgg aaggactcat gac 23

<210> 72  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       primer  
  
 <400> 72  
 gacttgccct tcgagtgacc gta 23

<210> 73  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Combined DNA/RNA Molecule:  
       Synthetic oligonucleotide  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide  
  
 <400> 73  
 cgagaugccu ucaucagcct t 21

<210> 74  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Combined DNA/RNA Molecule:  
       Synthetic oligonucleotide  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
       oligonucleotide  
  
 <400> 74  
 uguucuucug gaaguccagt t 21

<210> 75  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Combined DNA/RNA Molecule:  
 Synthetic oligonucleotide

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 75  
 ucgaaguacu cagcguaagt t

21

<210> 76  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 consensus peptide

<220>  
 <221> MOD\_RES  
 <222> (7)  
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<220>  
 <221> MOD\_RES  
 <222> (8)  
 <223> Thr or Ser

<400> 76  
 Arg His Gly Gly Arg His Xaa Xaa  
 1 5

<210> 77  
 <211> 13  
 <212> PRT  
 <213> Aplysia punctata

<220>  
 <221> MOD\_RES  
 <222> (1)  
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<400> 77  
 Xaa Gly Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys  
 1 5 10

<210> 78  
 <211> 88  
 <212> PRT  
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<220>  
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<220>  
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<220>  
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<220>  
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 <222> (69)  
 <223> variable amino acid

<220>  
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 <222> (77)  
 <223> variable amino acid

<400> 78  
 Met Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val  
   1                  5                  10                  15  
 His Ala Asp Gly Xaa Xaa Arg Asn Arg Arg Gln Cys Asn Arg Glu Val  
           20                  25                  30  
 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly  
           35                  40                  45  
 Ala Asn Ser Xaa Tyr Met Leu Arg Asp Ser Gly Xaa Asp Ile Ala Val  
   50                  55                  60  
 Phe Glu Tyr Ser Xaa Arg Val Gly Gly Arg Leu Phe Xaa Tyr Gln Leu  
   65                  70                  75                  80  
 Pro Asn Thr Pro Asp Val Asn Leu  
                   85